INPUT SET: S1441.raw

```
 1                              SEQUENCE LISTING
 2
 3    (1)     General Information:
 4
 5        (i) APPLICANTS: Adams, Thomas R. et al.
 6
 7       (ii)  TITLE OF INVENTION: Methods and Compositions for the
 8             Production of Stably Transformed, Fertile, Monocot Plants
 9             and Cells Thereof
10
11      (iii) NUMBER OF SEQUENCES: 13
12
13       (iv) CORRESPONDENCE ADDRESS:
14             (A)  ADDRESSEE: Arnold, White & Durkee
15             (B)  STREET: P.O. BOX 4433
16             (C)  CITY: Houston
17             (D)  STATE: TX
18             (E)  COUNTRY: USA
19             (F)  ZIP: 77210
20
21        (v) COMPUTER READABLE FORM:
22             (A)  MEDIUM TYPE: Floppy disk
23             (B)  COMPUTER: IBM PC compatible
24             (C)  OPERATING SYSTEM: PC-DOS/MS-DOS
25             (D)  SOFTWARE: Patent In Release #1.0, Version #1.25
26
27       (vi) CURRENT APPLICATION DATA:
28             (A)  APPLICATION NUMBER: unknown
29             (B)  FILING DATE: August 25, 1993
30             (C)  CLASSIFICATION: unknown
31
32    (viii)  ATTORNEY/AGENT INFORMATION:
33             (A)  NAME: Parker, David L.
34             (B)  REGISTRATION NUMBER: 32,165
35             (C)  REFERENCE/DOCKET NUMBER: DEKA:055/PAR
36
37       (ix) TELECOMMUNICATION INFORMATION:
38             (A)  TELEPHONE: 512-320-7200
39             (B)  TELEFAX: 512-474-7577
40             (C)  TELEX: NOT APPLICABLE
41
42
43    (2) INFORMATION FOR SEQ ID NO:1:
44
45        (i) SEQUENCE CHARACTERISTICS:
46             (A)   LENGTH: 15 amino acid residues
47             (B)   TYPE: amino acid
48             (C)   STRANDEDNESS: single
49             (D)   TOPOLOGY: linear
50
51       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
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INPUT SET: S1441.raw

```
52
53    Met Ala Thr Val Pro Glu Leu Asn Cys Glu Met Pro Pro Ser Asp
54     1               5                    10                  15
55
56
57    (2) INFORMATION FOR SEQ ID NO:2:
58
59        (i) SEQUENCE CHARACTERISTICS:
60            (A) LENGTH: 35 base pairs
61            (B) TYPE: nucleic acid
62            (C) STRANDEDNESS: single
63            (D) TOPOLOGY: linear
64
65       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
66
67    GAGGATCCGT CGACATGGTA AGCTTAGCGG GCCCC                          35
68
69
70    (2)   INFORMATION FOR SEQ ID NO:3:
71
72        (i) SEQUENCE CHARACTERISTICS:
73            (A) LENGTH: 29 base pairs
74            (B) TYPE: nucleic acid
75            (C) STRANDEDNESS: single
76            (D) TOPOLOGY: linear
77
78       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
79
80    GATCCGTCGA CCATGGCGCT TCAAGCTTC
81       29
82
83
84    (2) INFORMATION FOR SEQ ID NO:4:
85
86        (i) SEQUENCE CHARACTERISTICS:
87            (A) LENGTH: 29 base pairs
88            (B) TYPE: nucleic acid
89            (C) STRANDEDNESS: single
90            (D) TOPOLOGY: linear
91
92       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
93
94    GCAGCTGGTA CCGCGAAGTT CGAAGGGCT
95       29
96
97
98    (2) INFORMATION FOR SEQ ID NO:5:
99
100       (i) SEQUENCE CHARACTERISTICS:
101           (A) LENGTH: 49 base pairs
102           (B) TYPE: nucleic acid
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103   (C) STRANDEDNESS: single
104   (D) TOPOLOGY: linear
105
106   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
107
108   CTAGACAACA AAGCAGCAAC CATGGCCAGC ATGCAAGGCC TCATGCATC
109   49
110
111
112   (2) INFORMATION FOR SEQ ID NO:6:
113
114   (i) SEQUENCE CHARACTERISTICS:
115   (A) LENGTH: 49 base pairs
116   (B) TYPE: nucleic acid
117   (C) STRANDEDNESS: single
118   (D) TOPOLOGY: linear
119
120   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:
121
122   CCGGGATGCA TGAGGCCTTG CATGCTGGCC ATGGTTGCTG CTTTGTTGT
123   49
124
125
126   (2) INFORMATION FOR SEQ ID NO:7:
127
128   (i) SEQUENCE CHARACTERISTICS:
129   (A) LENGTH: 11 amino acid residues
130   (B) TYPE: amino acid
131   (C) STRANDEDNESS: single
132   (D) TOPOLOGY: linear
133
134   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:
135
136   Met Ala Ser Met Gln Gly Leu Met His Pro Gly
137   1   5   10
138
139
140   (2) INFORMATION FOR SEQ ID NO:8:
141
142   (i) SEQUENCE CHARACTERISTICS:
143   (A) LENGTH: 6 amino acid residues
144   (B) TYPE: amino acid
145   (C) STRANDEDNESS: single
146   (D) TOPOLOGY: linear
147
148   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:
149
150   Val Lys Cys Met Gln Val
151   1   5
152
153

```
154    (2) INFORMATION FOR SEQ ID NO:9:
155
156         (i)  SEQUENCE CHARACTERISTICS:
157              (A) LENGTH: 18 base pairs
158              (B) TYPE: nucleic acid
159              (C) STRANDEDNESS: single
160              (D) TOPOLOGY: linear
161
162         (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:
163
164    AAGUGAAGUG AAGUGAAG
165         18
166
167
168    (2) INFORMATION FOR SEQ ID NO:10:
169
170         (i)  SEQUENCE CHARACTERISTICS:
171              (A) LENGTH: 1845 base pairs
172              (B) TYPE: nucleic acid
173              (C) STRANDEDNESS: single
174              (D) TOPOLOGY: linear
175
176         (ii) MOLECULE TYPE: DNA (genomic)
177
178         (ix) FEATURE:
179              (A) NAME/KEY: CDS
180              (B) LOCATION: 1..1839
181
182         (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:
183
184    ATG GAT AAC AAT CCG AAC ATC AAT GAA TGC ATT CCT TAC AAT TGC CTC
185         48
186    Met Asp Asn Asn Pro Asn Ile Asn Glu Cys Ile Pro Tyr Asn Cys Leu
187     1               5                  10                  15
188
189    AGC AAC CCT GAA GTG GAA GTG CTG GGT GGC GAA CGC ATC GAA ACC GGT
190         96
191    Ser Asn Pro Glu Val Glu Val Leu Gly Gly Glu Arg Ile Glu Thr Gly
192                 20                  25                  30
193
194    TAC ACC CCA ATC GAT ATT TCC CTG TCC CTG ACC CAA TTT CTG CTG AGC
195        144
196    Tyr Thr Pro Ile Asp Ile Ser Leu Ser Leu Thr Gln Phe Leu Leu Ser
197             35                  40                  45
198
199    GAA TTT GTG CCC GGT GCT GGC TTT GTG CTG GGC CTG GTG GAT ATC ATC
200        192
201    Glu Phe Val Pro Gly Ala Gly Phe Val Leu Gly Leu Val Asp Ile Ile
202         50                  55                  60
203
204    TGG GGC ATT TTT GGT CCC TCC CAA TGG GAC GCC TTT CTG GTG CAA ATT
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RAW SEQUENCE LISTING
PATENT APPLICATION *US/08/113,561*

DATE: 09/07/93
TIME: 10:40:54

INPUT SET: S1441.raw

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205      240
206   Trp Gly Ile Phe Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile
207    65                70              75                  80
208
209   GAA CAG CTG ATT AAC CAA CGC ATC GAA GAA TTC GCT AGG AAC CAA GCC
210      288
211   Glu Gln Leu Ile Asn Gln Arg Ile Glu Glu Phe Ala Arg Asn Gln Ala
212                   85                  90                  95
213
214   ATT TCC CGC CTG GAA GGC CTG AGC AAT CTG TAC CAA ATT TAC GCC GAA
215      336
216   Ile Ser Arg Leu Glu Gly Leu Ser Asn Leu Tyr Gln Ile Tyr Ala Glu
217               100             105             110
218
219   TCC TTT CGC GAG TGG GAA GCC GAT CCT ACC AAT CCA GCC CTG CGC GAA
220      384
221   Ser Phe Arg Glu Trp Glu Ala Asp Pro Thr Asn Pro Ala Leu Arg Glu
222               115             120             125
223
224   GAG ATG CGC ATT CAA TTC AAT GAC ATG AAC AGC GCC CTG ACC ACC GCT
225      432
226   Glu Met Arg Ile Gln Phe Asn Asp Met Asn Ser Ala Leu Thr Thr Ala
227          130             135             140
228
229   ATT CCT CTG TTT GCC GTG CAA AAT TAC CAA GTG CCT CTG CTG TCC GTG
230      480
231   Ile Pro Leu Phe Ala Val Gln Asn Tyr Gln Val Pro Leu Leu Ser Val
232   145             150             155                 160
233
234   TAC GTG CAA GCT GCC AAT CTG CAT CTG TCC GTG CTG CGC GAT GTG TCC
235      528
236   Tyr Val Gln Ala Ala Asn Leu His Leu Ser Val Leu Arg Asp Val Ser
237                   165             170             175
238
239   GTG TTT GGC CAA AGG TGG GGC TTT GAT GCC GCC ACC ATC AAT AGC CGC
240      576
241   Val Phe Gly Gln Arg Trp Gly Phe Asp Ala Ala Thr Ile Asn Ser Arg
242               180             185             190
243
244   TAC AAT GAT CTG ACC AGG CTG ATT GGC AAC TAC ACC GAT TAC GCT GTG
245      624
246   Tyr Asn Asp Leu Thr Arg Leu Ile Gly Asn Tyr Thr Asp Tyr Ala Val
247               195             200             205
248
249   CGC TGG TAC AAT ACC GGC CTG GAA CGC GTG TGG GGC CCA GAT TCC CGC
250      672
251   Arg Trp Tyr Asn Thr Gly Leu Glu Arg Val Trp Gly Pro Asp Ser Arg
252      210             215             220
253
254   GAT TGG GTG AGG TAC AAT CAA TTT CGC CGC GAA CTG ACC CTG ACC GTG
255      720
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RAW SEQUENCE LISTING
PATENT APPLICATION *US/08/113,561*

DATE: 09/07/93
TIME: 10:40:55

INPUT SET: S1441.raw

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256    Asp Trp Val Arg Tyr Asn Gln Phe Arg Arg Glu Leu Thr Leu Thr Val
257    225             230             235             240
258
259    CTC GAT ATC GTG GCT CTG TTC CCA AAT TAC GAT AGC CGC CGC TAC CCA
260        768
261    Leu Asp Ile Val Ala Leu Phe Pro Asn Tyr Asp Ser Arg Arg Tyr Pro
262                245             250             255
263
264    ATT CGA ACC GTG TCC CAA CTG ACC CGC GAA ATT TAC ACC AAC CCA GTG
265        816
266    Ile Arg Thr Val Ser Gln Leu Thr Arg Glu Ile Tyr Thr Asn Pro Val
267                260             265             270
268
269    CTG GAA AAT TTT GAT GGT AGC TTT CGC GGC TCC GCT CAG GGC ATC GAA
270        864
271    Leu Glu Asn Phe Asp Gly Ser Phe Arg Gly Ser Ala Gln Gly Ile Glu
272                275             280             285
273
274    CGC AGC ATT AGG AGC CCA CAT CTG ATG GAT ATC CTG AAC AGC ATC ACC
275        912
276    Arg Ser Ile Arg Ser Pro His Leu Met Asp Ile Leu Asn Ser Ile Thr
277        290             295             300
278
279    ATC TAC ACC GAT GCT CAT AGG GGT TAC TAC TAC TGG TCC GGC CAT CAA
280        960
281    Ile Tyr Thr Asp Ala His Arg Gly Tyr Tyr Tyr Trp Ser Gly His Gln
282    305             310             315             320
283
284    ATC ATG GCT TCC CCT GTG GGC TTT TCC GGG CCA GAA TTC ACC TTT CCA
285        1008
286    Ile Met Ala Ser Pro Val Gly Phe Ser Gly Pro Glu Phe Thr Phe Pro
287                325             330             335
288
289    CTG TAC GGC ACG ATG GGC AAT GCC GCT CCA CAA CAA CGC ATT GTG GCT
290        1056
291    Leu Tyr Gly Thr Met Gly Asn Ala Ala Pro Gln Gln Arg Ile Val Ala
292                340             345             350
293
294    CAA CTG GGT CAG GGC GTG TAC CGC ACC CTG TCC TCC ACC CTG TAC CGC
295        1104
296    Gln Leu Gly Gln Gly Val Tyr Arg Thr Leu Ser Ser Thr Leu Tyr Arg
297                355             360             365
298
299    CGC CCT TTT AAT ATC GGC ATC AAC AAC CAG CAA CTG TCC GTG CTG GAC
300        1152
301    Arg Pro Phe Asn Ile Gly Ile Asn Asn Gln Gln Leu Ser Val Leu Asp
302        370             375             380
303
304    GGC ACC GAA TTT GCT TAC GGC ACC TCC TCC AAT CTG CCA TCC GCT GTA
305        1200
306    Gly Thr Glu Phe Ala Tyr Gly Thr Ser Ser Asn Leu Pro Ser Ala Val
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307   385                  390                 395                  400
308
309   TAC CGC AAG AGC GGC ACC GTG GAT TCC CTG GAT GAA ATC CCA CCA CAG
310      1248
311   Tyr Arg Lys Ser Gly Thr Val Asp Ser Leu Asp Glu Ile Pro Pro Gln
312              405         410                  415
313
314   AAT AAC AAC GTG CCA CCT AGG CAA GGC TTT AGC CAT CGC CTG AGC CAT
315      1296
316   Asn Asn Asn Val Pro Pro Arg Gln Gly Phe Ser His Arg Leu Ser His
317              420         425                  430
318
319   GTG TCC ATG TTT CGC TCC GGC TTT AGC AAT AGC AGC GTG AGC ATC ATC
320      1344
321   Val Ser Met Phe Arg Ser Gly Phe Ser Asn Ser Ser Val Ser Ile Ile
322              435         440                  445
323
324   CGC GCT CCT ATG TTC TCC TGG ATC CAT CGC AGC GCT GAA TTT AAC AAC
325      1392
326   Arg Ala Pro Met Phe Ser Trp Ile His Arg Ser Ala Glu Phe Asn Asn
327        450           455              460
328
329   ATC ATT GCC TCC GAT AGC ATT ACC CAA ATC CCT GCC GTG AAG GGC AAC
330      1440
331   Ile Ile Ala Ser Asp Ser Ile Thr Gln Ile Pro Ala Val Lys Gly Asn
332   465              470              475                  480
333
334   TTT CTG TTT AAT GGT TCC GTG ATT TCC GGC CCA GGC TTT ACC GGT GGC
335      1488
336   Phe Leu Phe Asn Gly Ser Val Ile Ser Gly Pro Gly Phe Thr Gly Gly
337              485              490                  495
338
339   GAC CTG GTG CGC CTG AAT AGC AGC GGC AAT AAC ATT CAG AAT CGC GGC
340      1536
341   Asp Leu Val Arg Leu Asn Ser Ser Gly Asn Asn Ile Gln Asn Arg Gly
342              500              505                  510
343
344   TAC ATT GAA GTG CCA ATT CAC TTC CCA TCC ACC TCC ACC CGC TAC CGC
345      1584
346   Tyr Ile Glu Val Pro Ile His Phe Pro Ser Thr Ser Thr Arg Tyr Arg
347              515              520                  525
348
349   GTG CGC GTG CGC TAC GCT TCC GTG ACC CCA ATT CAC CTC AAC GTT AAC
350      1632
351   Val Arg Val Arg Tyr Ala Ser Val Thr Pro Ile His Leu Asn Val Asn
352           530              535              540
353
354   TGG GGC AAT TCC TCC ATT TTT TCC AAT ACC GTG CCA GCT ACC GCT ACC
355      1680
356   Trp Gly Asn Ser Ser Ile Phe Ser Asn Thr Val Pro Ala Thr Ala Thr
357   545              550              555                  560
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358
359   TCC CTG GAT AAT CTG CAA TCC AGC GAT TTT GGT TAC TTT GAA AGC GCC
360      1728
361   Ser Leu Asp Asn Leu Gln Ser Ser Asp Phe Gly Tyr Phe Glu Ser Ala
362              565                 570                 575
363
364   AAT GCT TTT ACC TCC TCC CTG GGT AAT ATC GTG GGT GTG CGC AAT TTT
365      1776
366   Asn Ala Phe Thr Ser Ser Leu Gly Asn Ile Val Gly Val Arg Asn Phe
367              580                 585                 590
368
369   AGC GGC ACC GCC GGC GTG ATC ATC GAC CGC TTT GAA TTT ATT CCA GTG
370      1824
371   Ser Gly Thr Ala Gly Val Ile Ile Asp Arg Phe Glu Phe Ile Pro Val
372          595                 600                 605
373
374   ACC GCC ACC CTC GAG TAGGTA
375      1845
376   Thr Ala Thr Leu Glu
377      610
378
379   (2) INFORMATION FOR SEQ ID NO:11:
380
381          (i) SEQUENCE CHARACTERISTICS:
382              (A) LENGTH: 613 amino acids
383              (B) TYPE: amino acid
384              (D) TOPOLOGY: linear
385
386          (ii) MOLECULE TYPE: protein
387
388          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:
389
390   Met Asp Asn Asn Pro Asn Ile Asn Glu Cys Ile Pro Tyr Asn Cys Leu
391    1               5                  10                  15
392
393   Ser Asn Pro Glu Val Glu Val Leu Gly Gly Glu Arg Ile Glu Thr Gly
394              20                  25                  30
395
396   Tyr Thr Pro Ile Asp Ile Ser Leu Ser Leu Thr Gln Phe Leu Leu Ser
397          35                  40                  45
398
399   Glu Phe Val Pro Gly Ala Gly Phe Val Leu Gly Leu Val Asp Ile Ile
400          50                  55                  60
401
402   Trp Gly Ile Phe Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile
403    65                  70                  75                  80
404
405   Glu Gln Leu Ile Asn Gln Arg Ile Glu Glu Phe Ala Arg Asn Gln Ala
406              85                  90                  95
407
408   Ile Ser Arg Leu Glu Gly Leu Ser Asn Leu Tyr Gln Ile Tyr Ala Glu
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RAW SEQUENCE LISTING
PATENT APPLICATION   *US/08/113,561*

DATE: 09/07/93
TIME: 10:41:20

INPUT SET: S1441.raw

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409                   100                   105                   110
410
411   Ser Phe Arg Glu Trp Glu Ala Asp Pro Thr Asn Pro Ala Leu Arg Glu
412           115             120             125
413
414   Glu Met Arg Ile Gln Phe Asn Asp Met Asn Ser Ala Leu Thr Thr Ala
415        ·130             135             140
416
417   Ile Pro Leu Phe Ala Val Gln Asn Tyr Gln Val Pro Leu Leu Ser Val
418   145             150             155             160
419
420   Tyr Val Gln Ala Ala Asn Leu His Leu Ser Val Leu Arg Asp Val Ser
421           165             170             175
422
423   Val Phe Gly Gln Arg Trp Gly Phe Asp Ala Ala Thr Ile Asn Ser Arg
424           180             185             190
425
426   Tyr Asn Asp Leu Thr Arg Leu Ile Gly Asn Tyr Thr Asp Tyr Ala Val
427           195             200             205
428
429   Arg Trp Tyr Asn Thr Gly Leu Glu Arg Val Trp Gly Pro Asp Ser Arg
430           210             215             220
431
432   Asp Trp Val Arg Tyr Asn Gln Phe Arg Arg Glu Leu Thr Leu Thr Val
433   225             230             235             240
434
435   Leu Asp Ile Val Ala Leu Phe Pro Asn Tyr Asp Ser Arg Arg Tyr Pro
436           245             250             255
437
438   Ile Arg Thr Val Ser Gln Leu Thr Arg Glu Ile Tyr Thr Asn Pro Val
439           260             265             270
440
441   Leu Glu Asn Phe Asp Gly Ser Phe Arg Gly Ser Ala Gln Gly Ile Glu
442           275             280             285
443
444   Arg Ser Ile Arg Ser Pro His Leu Met Asp Ile Leu Asn Ser Ile Thr
445           290             295             300
446
447   Ile Tyr Thr Asp Ala His Arg Gly Tyr Tyr Tyr Trp Ser Gly His Gln
448   305             310             315             320
449
450   Ile Met Ala Ser Pro Val Gly Phe Ser Gly Pro Glu Phe Thr Phe Pro
451           325             330             335
452
453   Leu Tyr Gly Thr Met Gly Asn Ala Ala Pro Gln Gln Arg Ile Val Ala
454           340             345             350
455
456   Gln Leu Gly Gln Gly Val Tyr Arg Thr Leu Ser Ser Thr Leu Tyr Arg
457           355             360             365
458
459   Arg Pro Phe Asn Ile Gly Ile Asn Asn Gln Gln Leu Ser Val Leu Asp
```

```
460        370                   375                   380
461
462   Gly Thr Glu Phe Ala Tyr Gly Thr Ser Ser Asn Leu Pro Ser Ala Val
463   385                 390                   395                   400
464
465   Tyr Arg Lys Ser Gly Thr Val Asp Ser Leu Asp Glu Ile Pro Pro Gln
466             405                   410                   415
467
468   Asn Asn Asn Val Pro Pro Arg Gln Gly Phe Ser His Arg Leu Ser His
469             420                   425                   430
470
471   Val Ser Met Phe Arg Ser Gly Phe Ser Asn Ser Ser Val Ser Ile Ile
472             435                   440                   445
473
474   Arg Ala Pro Met Phe Ser Trp Ile His Arg Ser Ala Glu Phe Asn Asn
475             450                   455                   460
476
477   Ile Ile Ala Ser Asp Ser Ile Thr Gln Ile Pro Ala Val Lys Gly Asn
478   465                   470                   475                   480
479
480   Phe Leu Phe Asn Gly Ser Val Ile Ser Gly Pro Gly Phe Thr Gly Gly
481             485                   490                   495
482
483   Asp Leu Val Arg Leu Asn Ser Ser Gly Asn Asn Ile Gln Asn Arg Gly
484             500                   505                   510
485
486   Tyr Ile Glu Val Pro Ile His Phe Pro Ser Thr Ser Thr Arg Tyr Arg
487             515                   520                   525
488
489   Val Arg Val Arg Tyr Ala Ser Val Thr Pro Ile His Leu Asn Val Asn
490             530                   535                   540
491
492   Trp Gly Asn Ser Ser Ile Phe Ser Asn Thr Val Pro Ala Thr Ala Thr
493   545                   550                   555                   560
494
495   Ser Leu Asp Asn Leu Gln Ser Ser Asp Phe Gly Tyr Phe Glu Ser Ala
496             565                   570                   575
497
498   Asn Ala Phe Thr Ser Ser Leu Gly Asn Ile Val Gly Val Arg Asn Phe
499             580                   585                   590
500
501   Ser Gly Thr Ala Gly Val Ile Ile Asp Arg Phe Glu Phe Ile Pro Val
502             595                   600                   605
503
504   Thr Ala Thr Leu Glu
505       610
506
507   (2) INFORMATION FOR SEQ ID NO:12:
508
509       (i) SEQUENCE CHARACTERISTICS:
510           (A) LENGTH: 1848 base pairs
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```
511          (B) TYPE: nucleic acid
512          (C) STRANDEDNESS: single
513          (D) TOPOLOGY: linear
514
515      (ii) MOLECULE TYPE: DNA (genomic)
516
517      (ix) FEATURE:
518          (A) NAME/KEY: CDS
519          (B) LOCATION: 1..1842
520
521      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:
522
523   ATG GAT AAC AAT CCG AAC ATC AAT GAA TGC ATT CCT TAC AAT TGC CTC
524       48
525   Met Asp Asn Asn Pro Asn Ile Asn Glu Cys Ile Pro Tyr Asn Cys Leu
526    1               5              10              15
527
528   AGC AAC CCT GAA GTG GAA GTG CTG GGT GGC GAA CGC ATC GAA ACC GGT
529       96
530   Ser Asn Pro Glu Val Glu Val Leu Gly Gly Glu Arg Ile Glu Thr Gly
531              20              25              30
532
533   TAC ACC CCA ATC GAT ATT TCC CTG TCC CTG ACC CAA TTT CTG CTG AGC
534       144
535   Tyr Thr Pro Ile Asp Ile Ser Leu Ser Leu Thr Gln Phe Leu Leu Ser
536              35              40              45
537
538   GAA TTT GTG CCC GGT GCT GGC TTT GTG CTG GGC CTG GTG GAT ATC ATC
539       192
540   Glu Phe Val Pro Gly Ala Gly Phe Val Leu Gly Leu Val Asp Ile Ile
541          50              55              60
542
543   TGG GGC ATT TTT GGT CCC TCC CAA TGG GAC GCC TTT CTG GTG CAA ATT
544       240
545   Trp Gly Ile Phe Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile
546    65              70              75              80
547
548   GAA CAG CTG ATT AAC CAA CGC ATC GAA GAA TTC GCT AGG AAC CAA GCC
549       288
550   Glu Gln Leu Ile Asn Gln Arg Ile Glu Glu Phe Ala Arg Asn Gln Ala
551                  85              90              95
552
553   ATT TCC CGC CTG GAA GGC CTG AGC AAT CTG TAC CAA ATT TAC GCC GAA
554       336
555   Ile Ser Arg Leu Glu Gly Leu Ser Asn Leu Tyr Gln Ile Tyr Ala Glu
556              100             105             110
557
558   TCC TTT CGC GAG TGG GAA GCC GAT CCT ACC AAT CCA GCC CTG CGC GAA
559       384
560   Ser Phe Arg Glu Trp Glu Ala Asp Pro Thr Asn Pro Ala Leu Arg Glu
561              115             120             125
```

```
562
563    GAG ATG CGC ATT CAA TTC AAT GAC ATG AAC AGC GCC CTG ACC ACC GCT
564       432
565    Glu Met Arg Ile Gln Phe Asn Asp Met Asn Ser Ala Leu Thr Thr Ala
566       130                 135               140
567
568    ATT CCT CTG TTT GCC GTG CAA AAT TAC CAA GTG CCT CTG CTG TCC GTG
569       480
570    Ile Pro Leu Phe Ala Val Gln Asn Tyr Gln Val Pro Leu Leu Ser Val
571    145                 150               155                   160
572
573    TAC GTG CAA GCT GCC AAT CTG CAT CTG TCC GTG CTG CGC GAT GTG TCC
574       528
575    Tyr Val Gln Ala Ala Asn Leu His Leu Ser Val Leu Arg Asp Val Ser
576                 165               170               175
577
578    GTG TTT GGC CAA AGG TGG GGC TTT GAT GCC GCC ACC ATC AAT AGC CGC
579       576
580    Val Phe Gly Gln Arg Trp Gly Phe Asp Ala Ala Thr Ile Asn Ser Arg
581                 180               185               190
582
583    TAC AAT GAT CTG ACC AGG CTG ATT GGC AAC TAC ACC GAT TAC GCT GTG
584       624
585    Tyr Asn Asp Leu Thr Arg Leu Ile Gly Asn Tyr Thr Asp Tyr Ala Val
586                 195               200               205
587
588    CGC TGG TAC AAT ACC GGC CTG GAA CGC GTG TGG GGC CCA GAT TCC CGC
589       672
590    Arg Trp Tyr Asn Thr Gly Leu Glu Arg Val Trp Gly Pro Asp Ser Arg
591       210               215               220
592
593    GAT TGG GTG AGG TAC AAT CAA TTT CGC CGC GAA CTG ACC CTG ACC GTG
594       720
595    Asp Trp Val Arg Tyr Asn Gln Phe Arg Arg Glu Leu Thr Leu Thr Val
596    225               230               235                   240
597
598    CTC GAT ATC GTG GCT CTG TTC CCA AAT TAC GAT AGC CGC CGC TAC CCA
599       768
600    Leu Asp Ile Val Ala Leu Phe Pro Asn Tyr Asp Ser Arg Arg Tyr Pro
601                 245               250               255
602
603    ATT CGA ACC GTG TCC CAA CTG ACC CGC GAA ATT TAC ACC AAC CCA GTG
604       816
605    Ile Arg Thr Val Ser Gln Leu Thr Arg Glu Ile Tyr Thr Asn Pro Val
606                 260               265               270
607
608    CTG GAA AAT TTT GAT GGT AGC TTT CGC GGC TCC GCT CAG GGC ATC GAA
609       864
610    Leu Glu Asn Phe Asp Gly Ser Phe Arg Gly Ser Ala Gln Gly Ile Glu
611                 275               280               285
612
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613    CGC AGC ATT AGG AGC CCA CAT CTG ATG GAT ATC CTG AAC AGC ATC ACC
614       912
615    Arg Ser Ile Arg Ser Pro His Leu Met Asp Ile Leu Asn Ser Ile Thr
616       290             295             300
617
618    ATC TAC ACC GAT GCT CAT AGG GGT TAC TAC TAC TGG TCC GGC CAT CAA
619       960
620    Ile Tyr Thr Asp Ala His Arg Gly Tyr Tyr Tyr Trp Ser Gly His Gln
621    305             310             315                 320
622
623    ATC ATG GCT TCC CCT GTG GGC TTT TCC GGG CCA GAA TTC ACC TTT CCA
624       1008
625    Ile Met Ala Ser Pro Val Gly Phe Ser Gly Pro Glu Phe Thr Phe Pro
626                325             330                 335
627
628    CTG TAC GGC ACG ATG GGC AAT GCC GCT CCA CAA CAA CGC ATT GTG GCT
629       1056
630    Leu Tyr Gly Thr Met Gly Asn Ala Ala Pro Gln Gln Arg Ile Val Ala
631                340             345                 350
632
633    CAA CTG GGT CAG GGC GTG TAC CGC ACC CTG TCC TCC ACC CTG TAC CGC
634       1104
635    Gln Leu Gly Gln Gly Val Tyr Arg Thr Leu Ser Ser Thr Leu Tyr Arg
636                355             360                 365
637
638    CGC CCT TTT AAT ATC GGC ATC AAC AAC CAG CAA CTG TCC GTG CTG GAC
639       1152
640    Arg Pro Phe Asn Ile Gly Ile Asn Asn Gln Gln Leu Ser Val Leu Asp
641       370             375             380
642
643    GGC ACC GAA TTT GCT TAC GGC ACC TCC TCC AAT CTG CCA TCC GCT GTA
644       1200
645    Gly Thr Glu Phe Ala Tyr Gly Thr Ser Ser Asn Leu Pro Ser Ala Val
646    385             390             395                 400
647
648    TAC CGC AAG AGC GGC ACC GTG GAT TCC CTG GAT GAA ATC CCA CCA CAG
649       1248
650    Tyr Arg Lys Ser Gly Thr Val Asp Ser Leu Asp Glu Ile Pro Pro Gln
651                405             410                 415
652
653    AAT AAC AAC GTG CCA CCT AGG CAA GGC TTT AGC CAT CGC CTG AGC CAT
654       1296
655    Asn Asn Asn Val Pro Pro Arg Gln Gly Phe Ser His Arg Leu Ser His
656                420             425                 430
657
658    GTG TCC ATG TTT CGC TCC GGC TTT AGC AAT AGC AGC GTG AGC ATC ATC
659       1344
660    Val Ser Met Phe Arg Ser Gly Phe Ser Asn Ser Ser Val Ser Ile Ile
661                435             440                 445
662
663    CGC GCT CCT ATG TTC TCC TGG ATC CAC CGC TCC GCT GAG TTC AAC AAC
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664     1392
665     Arg Ala Pro Met Phe Ser Trp Ile His Arg Ser Ala Glu Phe Asn Asn
666        450             455          460
667
668     ATC ATC CCG TCC TCC CAA ATC ACC CAA ATC CCG CTC ACC AAG TCC ACG
669     1440
670     Ile Ile Pro Ser Ser Gln Ile Thr Gln Ile Pro Leu Thr Lys Ser Thr
671     465             470          475             480
672
673     AAC CTC GGC TCC GGC ACG TCC GTC GTC AAG GGC CCG GGC TTC ACC GGC
674     1488
675     Asn Leu Gly Ser Gly Thr Ser Val Val Lys Gly Pro Gly Phe Thr Gly
676                485             490             495
677
678     GGC GAC ATC CTC CGC CGC ACG TCC CCG GGC CAG ATC TCC ACC CTC CGC
679     1536
680     Gly Asp Ile Leu Arg Arg Thr Ser Pro Gly Gln Ile Ser Thr Leu Arg
681            500             505             510
682
683     GTC AAC ATC ACG GCT CCG CTG AGC CAG CGC TAC AGG GTG CGC ATC AGA
684     1584
685     Val Asn Ile Thr Ala Pro Leu Ser Gln Arg Tyr Arg Val Arg Ile Arg
686            515             520             525
687
688     TAC GCT AGC ACG ACC AAC CTG CAA TTC CAC ACG TCC ATC GAC GGC AGA
689     1632
690     Tyr Ala Ser Thr Thr Asn Leu Gln Phe His Thr Ser Ile Asp Gly Arg
691        530             535             540
692
693     CCG ATC AAC CAG GGC AAC TTC AGC GCG ACG ATG AGC TCC GGG TCC AAC
694     1680
695     Pro Ile Asn Gln Gly Asn Phe Ser Ala Thr Met Ser Ser Gly Ser Asn
696     545             550             555             560
697
698     CTC CAG TCC GGC TCC TTC CGC ACG GTC GGT TTC ACC ACG CCG TTC AAC
699     1728
700     Leu Gln Ser Gly Ser Phe Arg Thr Val Gly Phe Thr Thr Pro Phe Asn
701                565             570             575
702
703     TTC TCC AAC GGC TCC TCC GTC TTC ACG CTC TCC GCT CAC GTC TTC AAC
704     1776
705     Phe Ser Asn Gly Ser Ser Val Phe Thr Leu Ser Ala His Val Phe Asn
706                580             585             590
707
708     TCC GGC AAC GAG GTG TAC ATC GAC CGC ATC GAG TTC GTC CCG GCC GAG
709     1824
710     Ser Gly Asn Glu Val Tyr Ile Asp Arg Ile Glu Phe Val Pro Ala Glu
711            595             600             605
712
713     GTC ACC TTC GAG CTC GAG TAGGTA
714     1848
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715    Val Thr Phe Glu Leu Glu
716        610
717
718
719    (2) INFORMATION FOR SEQ ID NO:13:
720
721         (i) SEQUENCE CHARACTERISTICS:
722             (A) LENGTH: 614 amino acids
723             (B) TYPE: amino acid
724             (D) TOPOLOGY: linear
725
726        (ii) MOLECULE TYPE: protein
727
728        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:
729
730    Met Asp Asn Asn Pro Asn Ile Asn Glu Cys Ile Pro Tyr Asn Cys Leu
731      1                 5                 10                15
732
733    Ser Asn Pro Glu Val Glu Val Leu Gly Gly Glu Arg Ile Glu Thr Gly
734            20                  25                  30
735
736    Tyr Thr Pro Ile Asp Ile Ser Leu Ser Leu Thr Gln Phe Leu Leu Ser
737            35                  40                  45
738
739    Glu Phe Val Pro Gly Ala Gly Phe Val Leu Gly Leu Val Asp Ile Ile
740        50                  55                  60
741
742    Trp Gly Ile Phe Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile
743     65                  70                  75                  80
744
745    Glu Gln Leu Ile Asn Gln Arg Ile Glu Glu Phe Ala Arg Asn Gln Ala
746                85                  90                  95
747
748    Ile Ser Arg Leu Glu Gly Leu Ser Asn Leu Tyr Gln Ile Tyr Ala Glu
749            100                 105                 110
750
751    Ser Phe Arg Glu Trp Glu Ala Asp Pro Thr Asn Pro Ala Leu Arg Glu
752            115                 120                 125
753
754    Glu Met Arg Ile Gln Phe Asn Asp Met Asn Ser Ala Leu Thr Thr Ala
755        130                 135                 140
756
757    Ile Pro Leu Phe Ala Val Gln Asn Tyr Gln Val Pro Leu Leu Ser Val
758    145                 150                 155                 160
759
760    Tyr Val Gln Ala Ala Asn Leu His Leu Ser Val Leu Arg Asp Val Ser
761                165                 170                 175
762
763    Val Phe Gly Gln Arg Trp Gly Phe Asp Ala Ala Thr Ile Asn Ser Arg
764                180                 185                 190
765
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766    Tyr Asn Asp Leu Thr Arg Leu Ile Gly Asn Tyr Thr Asp Tyr Ala Val
767        195             200             205
768
769    Arg Trp Tyr Asn Thr Gly Leu Glu Arg Val Trp Gly Pro Asp Ser Arg
770        210             215             220
771
772    Asp Trp Val Arg Tyr Asn Gln Phe Arg Arg Glu Leu Thr Leu Thr Val
773    225             230             235             240
774
775    Leu Asp Ile Val Ala Leu Phe Pro Asn Tyr Asp Ser Arg Arg Tyr Pro
776                245             250             255
777
778    Ile Arg Thr Val Ser Gln Leu Thr Arg Glu Ile Tyr Thr Asn Pro Val
779            260             265             270
780
781    Leu Glu Asn Phe Asp Gly Ser Phe Arg Gly Ser Ala Gln Gly Ile Glu
782        275             280             285
783
784    Arg Ser Ile Arg Ser Pro His Leu Met Asp Ile Leu Asn Ser Ile Thr
785        290             295             300
786
787    Ile Tyr Thr Asp Ala His Arg Gly Tyr Tyr Tyr Trp Ser Gly His Gln
788    305             310             315             320
789
790    Ile Met Ala Ser Pro Val Gly Phe Ser Gly Pro Glu Phe Thr Phe Pro
791                325             330             335
792
793    Leu Tyr Gly Thr Met Gly Asn Ala Ala Pro Gln Gln Arg Ile Val Ala
794            340             345             350
795
796    Gln Leu Gly Gln Gly Val Tyr Arg Thr Leu Ser Ser Thr Leu Tyr Arg
797        355             360             365
798
799    Arg Pro Phe Asn Ile Gly Ile Asn Asn Gln Gln Leu Ser Val Leu Asp
800        370             375             380
801
802    Gly Thr Glu Phe Ala Tyr Gly Thr Ser Ser Asn Leu Pro Ser Ala Val
803    385             390             395             400
804
805    Tyr Arg Lys Ser Gly Thr Val Asp Ser Leu Asp Glu Ile Pro Pro Gln
806                405             410             415
807
808    Asn Asn Asn Val Pro Pro Arg Gln Gly Phe Ser His Arg Leu Ser His
809                420             425             430
810
811    Val Ser Met Phe Arg Ser Gly Phe Ser Asn Ser Ser Val Ser Ile Ile
812        435             440             445
813
814    Arg Ala Pro Met Phe Ser Trp Ile His Arg Ser Ala Glu Phe Asn Asn
815        450             455             460
816
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817    Ile Ile Pro Ser Ser Gln Ile Thr Gln Ile Pro Leu Thr Lys Ser Thr
818    465             470             475             480
819
820    Asn Leu Gly Ser Gly Thr Ser Val Val Lys Gly Pro Gly Phe Thr Gly
821                    485             490             495
822
823    Gly Asp Ile Leu Arg Arg Thr Ser Pro Gly Gln Ile Ser Thr Leu Arg
824            500             505             510
825
826    Val Asn Ile Thr Ala Pro Leu Ser Gln Arg Tyr Arg Val Arg Ile Arg
827        515             520             525
828
829    Tyr Ala Ser Thr Thr Asn Leu Gln Phe His Thr Ser Ile Asp Gly Arg
830        530             535             540
831
832    Pro Ile Asn Gln Gly Asn Phe Ser Ala Thr Met Ser Ser Gly Ser Asn
833    545             550             555             560
834
835    Leu Gln Ser Gly Ser Phe Arg Thr Val Gly Phe Thr Thr Pro Phe Asn
836                    565             570             575
837
838    Phe Ser Asn Gly Ser Ser Val Phe Thr Leu Ser Ala His Val Phe Asn
839            580             585             590
840
841    Ser Gly Asn Glu Val Tyr Ile Asp Arg Ile Glu Phe Val Pro Ala Glu
842            595             600             605
843
844    Val Thr Phe Glu Leu Glu
845        610
846
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SEQUENCE VERIFICATION REPORT
PATENT APPLICATION *US/08/113,561*

INPUT SET: S1441.raw

Line	Error	Original Text
28	Wrong application Serial Number	(A) APPLICATION NUMBER: unknown
29	Wrong Filing Date	(B) FILING DATE: August 25, 1993
30	Wrong Classification	(C) CLASSIFICATION: unknown
78	Entered (29) and Calc. Seq. Length (0) differ	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
92	Entered (29) and Calc. Seq. Length (0) differ	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
106	Entered (49) and Calc. Seq. Length (0) differ	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
120	Entered (49) and Calc. Seq. Length (0) differ	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:
162	Entered (18) and Calc. Seq. Length (0) differ	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:
182	Entered (1845) and Calc. Seq. Length (0) differ	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:
521	Entered (1848) and Calc. Seq. Length (0) differ	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

SEQUENCE MISSING ITEM REPORT
PATENT APPLICATION   *US/08/113,561*

INPUT SET: S1441.raw

APPLICATION NUMBER
FILING DATE
PRIOR APPLICATION DATA

SEQUENCE CORRECTION REPORT
PATENT APPLICATION *US/08/113,561*

INPUT SET: S1441.raw

Line	Original Text	Corrected Text
5	(i) APPLICANTS: Adams, Thomas R. et al.	(i) APPLICANT: Adams, Thomas R. et al.